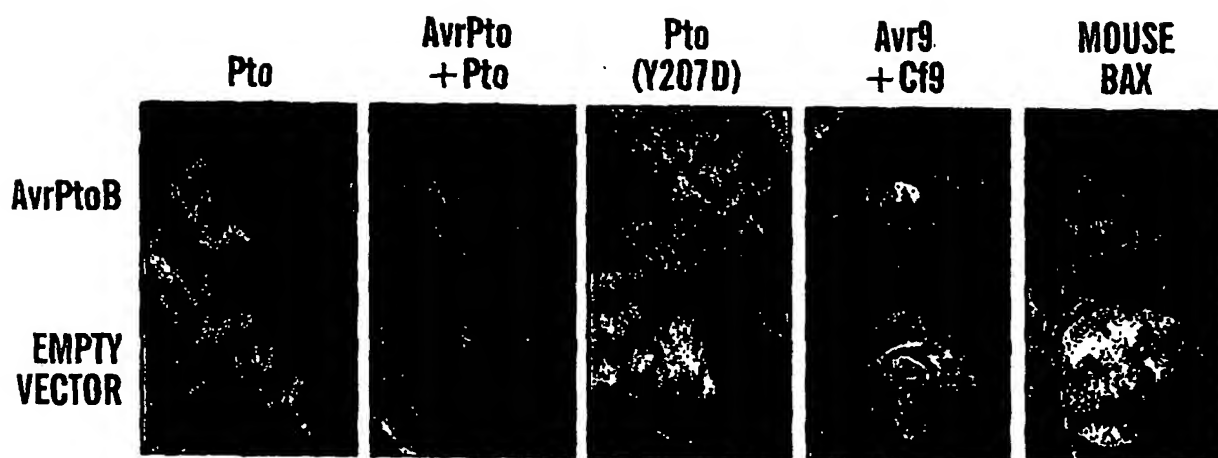


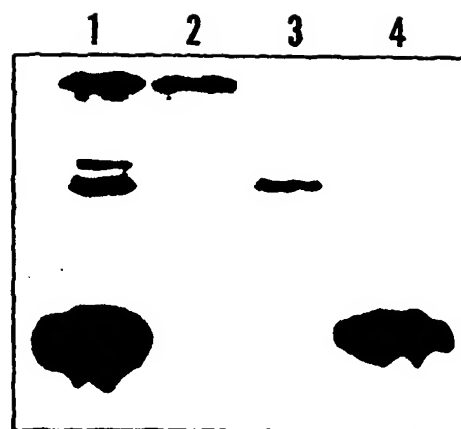
1/22



**FIG. 1A**

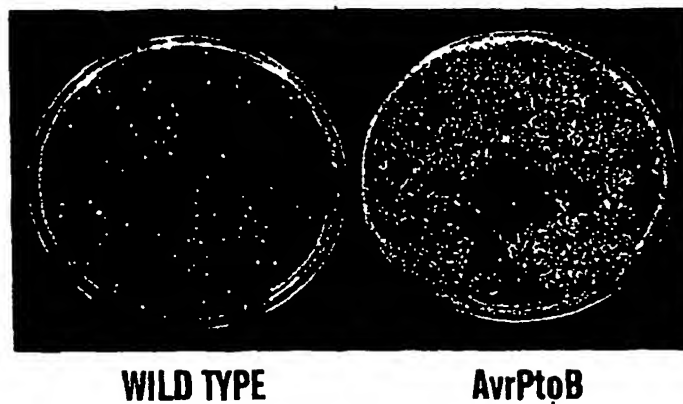


**FIG. 1B**

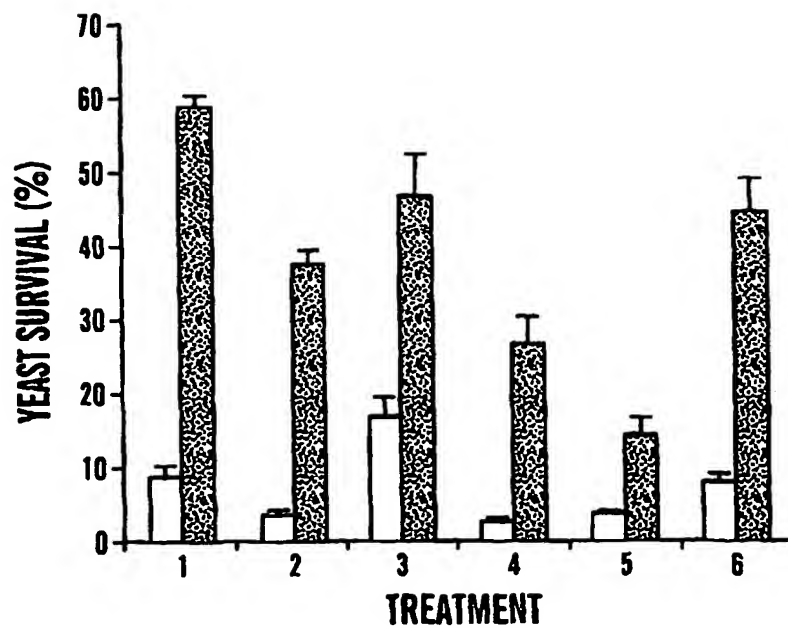


**FIG. 1C**

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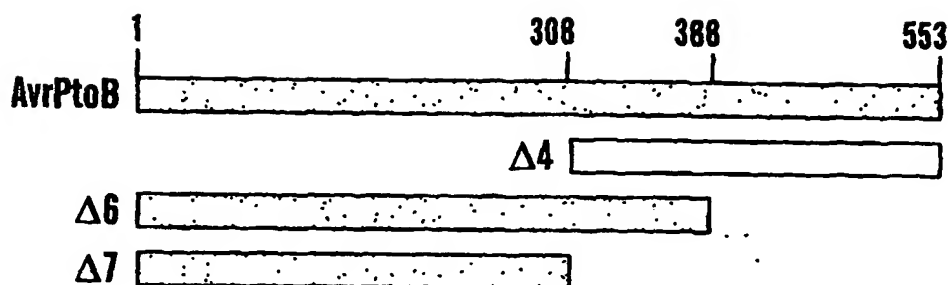


**FIG. 2A**



**FIG. 2B**

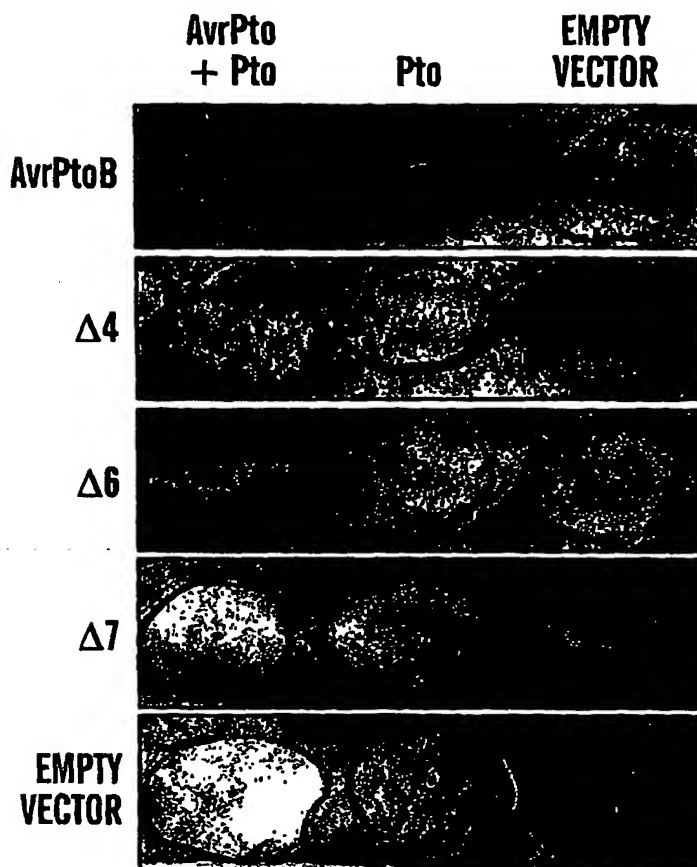
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**FIG. 3A**

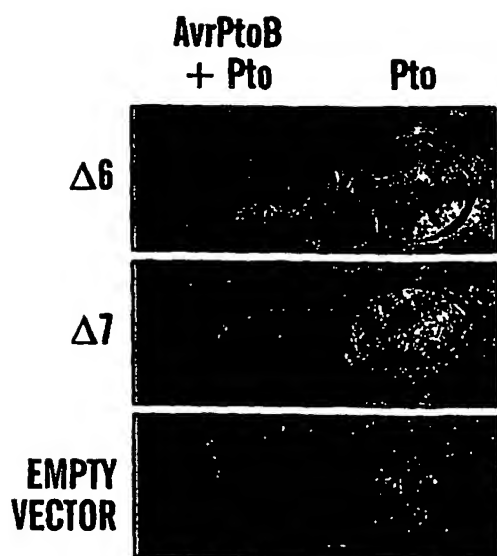
	RG-PtoR (Pto/Pto, Prf/Prf)	RG-Prf3 (Pto/Pto, Prf3/Prf3)	RG-Pto11 (pto11/pto11, Prf/Prf)	RG-ptoS (pto/pto, Prf/Prf)
AvrPtoB	+	-	-	-
Δ4	-	-	-	-
Δ6	+	-	+	-*
Δ7	+	-	-	-

**FIG. 3B**

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**FIG. 4A**

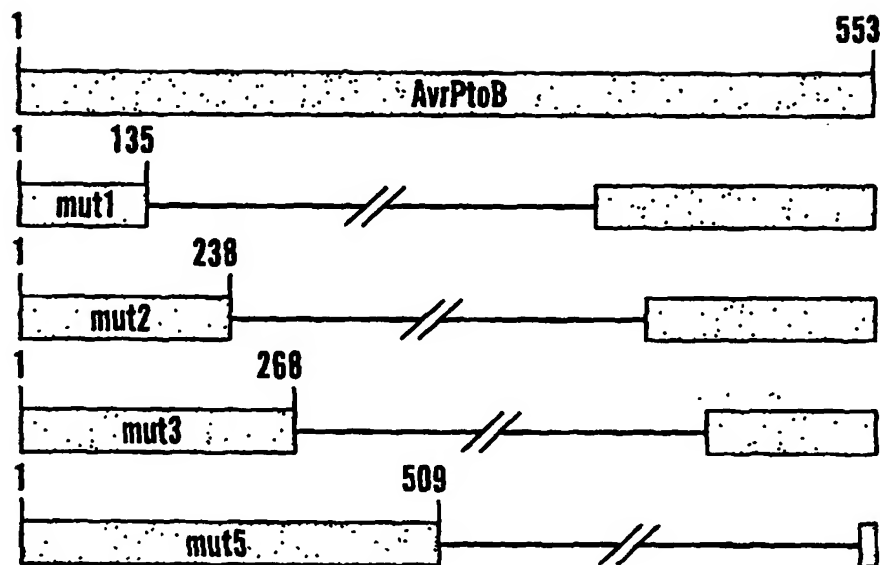


**FIG. 4B**



**FIG. 4C**

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**FIG. 5A**

	RG-PtoR (Pto/Pto, Prf/Prf)	RG-prf3 (Pto/Pto, prf3/prf3)	RG-pto11 (pto11/pto11, Prf/Prf)	RG-ptoS (pto/pto, Prf/Prf)
AvrPtoB	I	D	D	D
mut1	I	D	D	D
mut2	I	D	D	D
mut3	I	D	D	D
mut5	I	D	I	D

**FIG. 5B**

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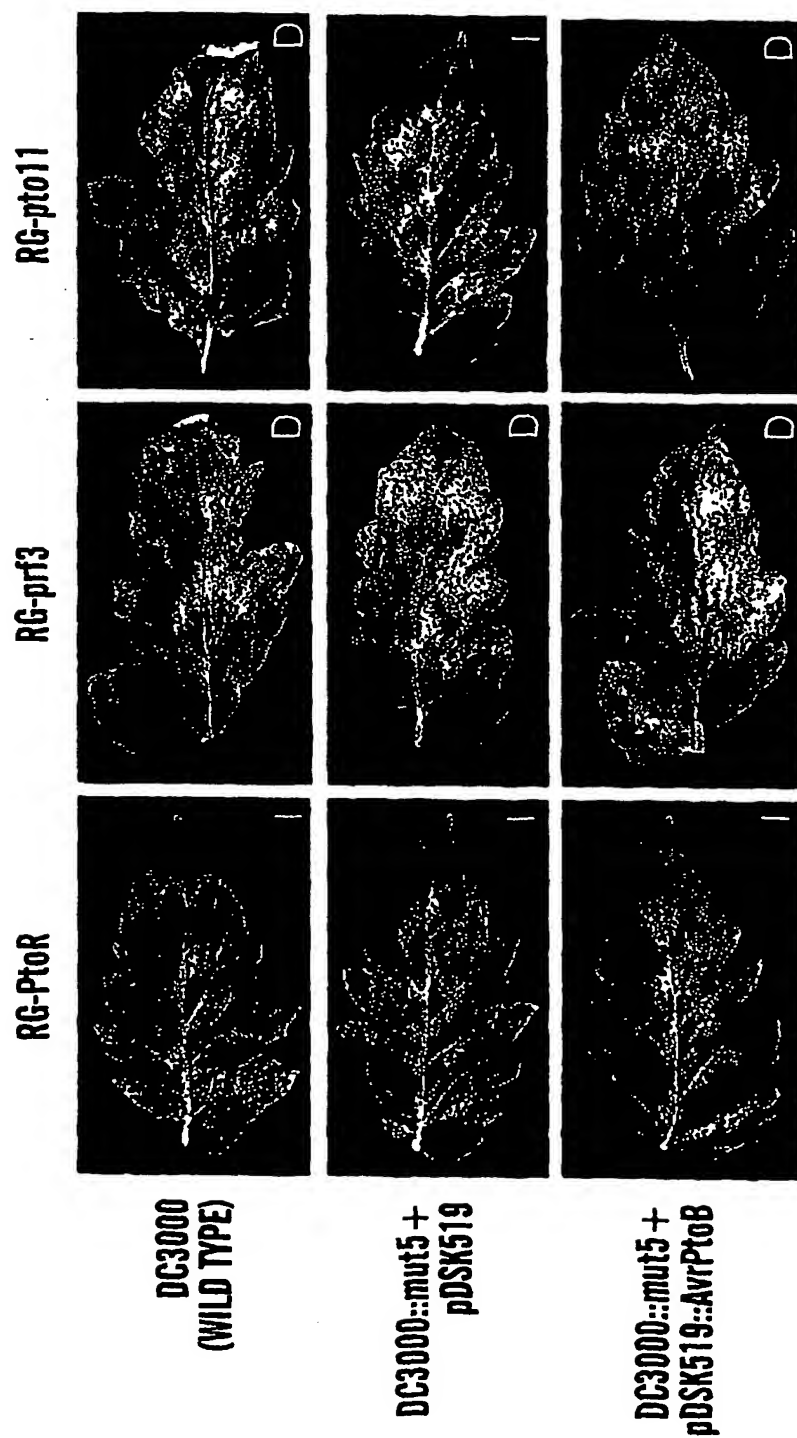
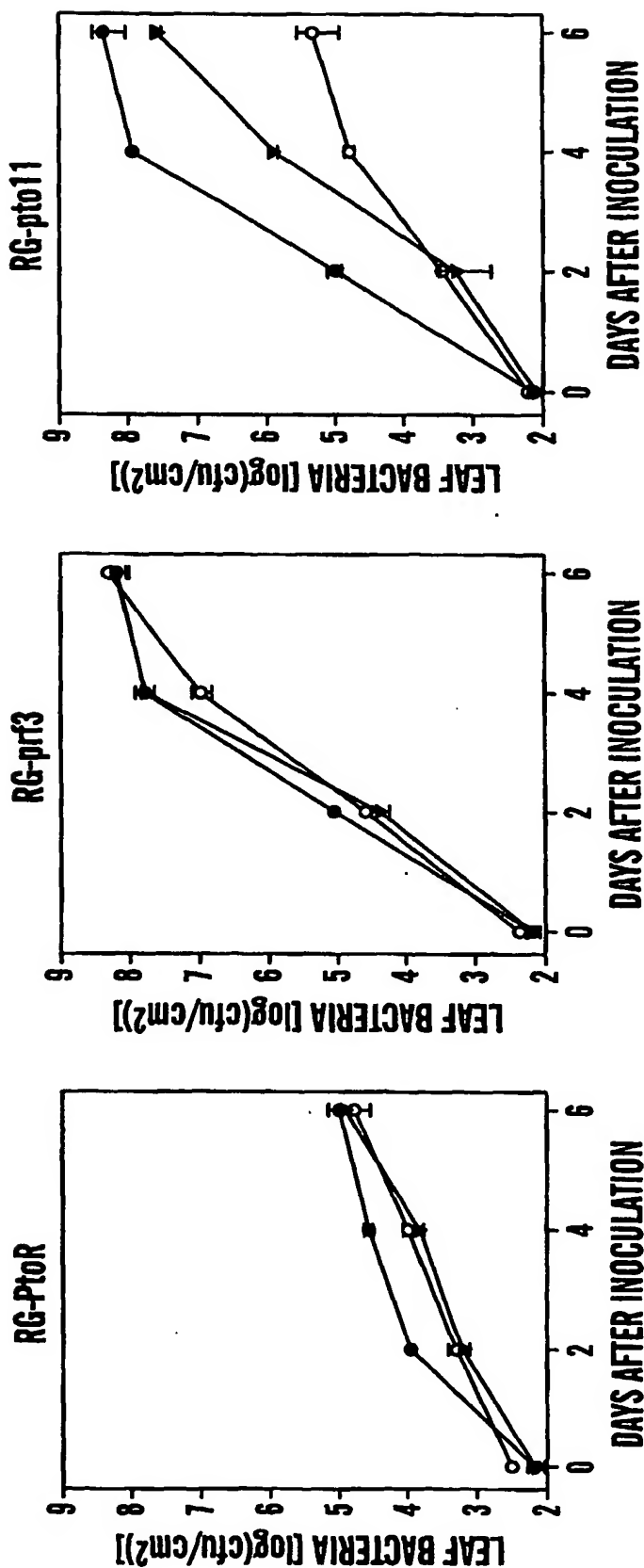


FIG. 6A

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- DC3000
- DC3000::mut5 + pDSK519
- ▼ DC3000::mut5 + pDSK519::avrPtoB



**FIG. 6B**

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M A G I N G A G P S G A Y F V G H T D P Majority										- R E M L L R A R P L S R Q T R E W V A Majority									
20										70									
M A G I N R A G P S G A Y F V G H T D P DC3000										G R E R L S R S T A L S R Q T R E W L E DC3000									
M A G I N G A G P S G A Y F V G H T D P T1										- R E M L L R A R P L S R Q T R E W V A T1									
M A G I N G A G P S G A Y F V G H T D P PT23										- R E M L L R A R P L S R Q T R E W V A PT23									
M A G I N G A G P S G A Y F V G H T D P JL1065										- R E M L L R A R P L S R Q T R E W V A JL1065									
E P A S G G A H G S S S G A S S S N S P Majority										Q G M P P T A E A G V P I R P Q E S A E Majority									
30										90									
E P V S G G Q A H G S G S G A S S S N S P DC3000										Q G M P P T A E D A S V R R R R P Q V T A D DC3000									
E P A S G G A H G S S S G A R S S S N S P T1										Q G M P P T A E A G V P I R P Q E S A E T1									
E P A S G G A H G S S S G A S S S N S P PT23										Q G M P P T A E A G V P I R P Q E S A E PT23									
E P A S G G A H G S S S G A S S S N S P JL1065										Q G M P P T A E A G V P I R P Q L S A E JL1065									
R L - P A P P D A P A S Q A R D R - - - Majority										A A A P Q A R A E E R H T P E A D A A A Majority									
50										110									
Q V Q P R P S N T P P S N A P A P P T DC3000										A A T P - - R A E A R R T P E A T A D A DC3000									
R L - P A P P D A P A S Q A R D R - - - T1										A A A P Q A R A L E R H I P E A D A A A T1									
R L - P A P P D A P A S Q A R D R - - - PT23										A A A P Q A R A L C R H T P E A D A A A PT23									
R L - P A P P D A P A S Q A R D R - - - JL1065										A A A P Q A R A L E R H T P E A D A A A JL1065									
60										120									

FIG. 7A



**PCT/US2003/025247**

**FIG. 7B**

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RSTVPPPTSTESSGSGSNQRTL Majority		-GANRVVMRRNHGNN EADA - Majority	
250		310	
215	- - - P A S P A A S S S G S S Q R S L	268	- R V D R A A M R N R G N D E A D A - -
236	R S T V P P T S T L S S S G S S Q R T L	296	- G A N R V V M R N H G N N E A D A - -
236	R S T V P P T S T L S S S G S S Q R T L	296	- G A N R V V M R N H G N N E A D A - -
236	R S T V P P T S T L S S S G S S Q R T L	296	- G A N R V V M R N H G N N E A D A - -
270		330	
LGRFAGLMTPNQRRPSSASN Majority		ALQGLAQQGVDMEDLRAALE Majority	
231	FGRFA R L W A P N Q G R S - - - N	285	A L R G L V Q Q G V N L E H L R T A L E
256	LGRFAGLWIPNQRRPSSASN	313	A L Q G L A Q Q G V D M E D L R A A L E
256	LGRFAGLWIPNQRRPSSASN	313	A L Q G L A Q Q G V D M E D L R A A L E
256	LGRFAGLWIPNQRRPSSASN	313	A L Q G L A Q Q G V D M E D L R A A L E
290		350	
ASASQRPVDRSPPRVNQVPTI Majority		RHILHRRRPIPM D I A Y A L Q G V Majority	
248	T A S Q T P V D R S P P R V N Q R P I	305	R H V M Q R L P I P L D I G S A L Q N V
276	A S A S Q R P V D R S P P R V N Q V P I	333	R H I L H R R R P I P M D I A Y A L Q G V
276	A S A S Q R P V D R S P P R V N Q V P I	333	R H I L H R R R P I P M D I A Y A L Q G V
276	A S A S Q R P V D R S P P R V N Q V P I	333	R H I L H R R R P I P M D I A Y A L Q G V
300		360	
T A S Q T P V D R S P P R V N Q R P I		RHV M Q R L P I P L D I G S A L Q N V	
276	A S A S Q R P V D R S P P R V N Q V P I	305	R H I L H R R R P I P M D I A Y A L Q G V
276	A S A S Q R P V D R S P P R V N Q V P I	333	R H I L H R R R P I P M D I A Y A L Q G V
276	A S A S Q R P V D R S P P R V N Q V P I	333	R H I L H R R R P I P M D I A Y A L Q G V

FIG. 7C

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G I A P S I D T G E S L M E N P L M N L Majority		L Q V I P A R E D Y E N N V A Y G V R L Majority	
325	G I N P S I D L G E S L V Q H P L L N L	430	L R V M E R E D Y E N N V A Y G V R L
353	G I A P S I D T G E S L M E N P L M N L	440	L Q V I P A R E D Y E N N V A Y G V R L
353	G I A P S I D T G E S L M E N P L M N L		L Q V I P A R E D Y E N N V A Y G V R L
353	G I A P S I D T G E S L M E N P L M N L		L Q V I P A R E D Y E N N V A Y G V R L
	S V A L H R A L G P R P A R A Q A P R P Majority		L S L N P G A G V R E T V A A F V N N R Majority
345	N V A L N R M L G L R P P S A E R A P R P	450	L N L N P G V G V R Q A V A A F V T D R
373	S V A L H R A L G P R P A R A Q A P R P		L S L N P G A G V R E T V A A F V N N R
373	S V A L H R A L G P R P A R A Q A P R P		L S L N P G A G V R E T V A A F V N N R
373	S V A L H R A L G P R P A R A Q A P R P		L S L N P G A G V R E T V A A F V N N R
	A V P V A P A T V S R R P D S A R A T R Majority		Y E R Q A V V A D I R A A L N - L S K Q Majority
365	A V P V A P A T A S R R R P D G T R A T R	470	A E R P A V V A N I R A A L D P I A S Q
393	A V P V A P A T V S R R R P D S A R A T R		Y E R Q A V V A D I R A A L N - L S K Q
393	A V P V A P A T V S R R R P D S A R A T R		Y E R Q A V V A D I R A A L N - L S K Q
393	A V P V A P A T V S R R R P D S A R A T R		Y E R Q A V V A D I R A A L N - L S K Q

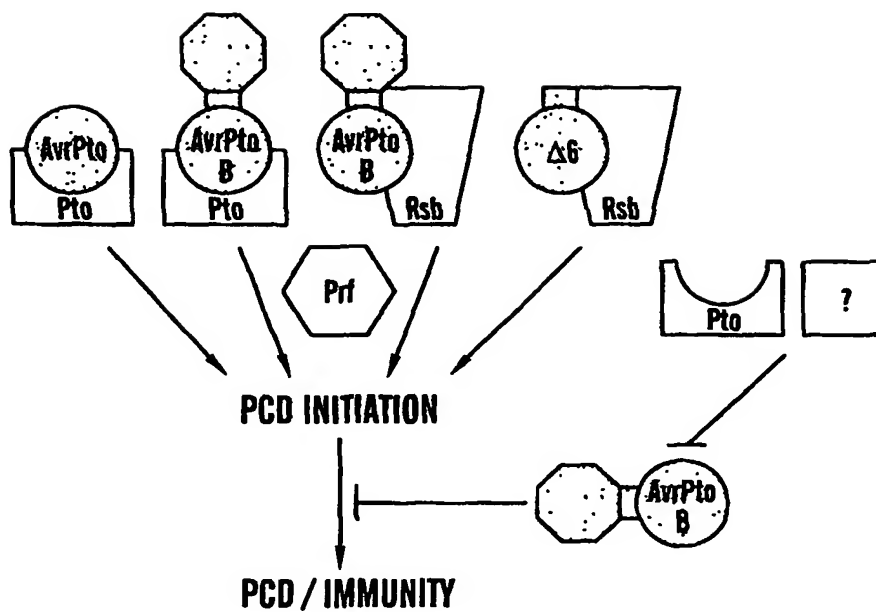
FIG. 7D

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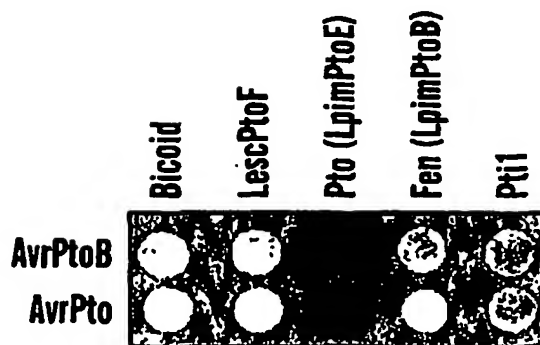
F N K L R T V S K A D A A S N K P G F K Majority		S Y S R E A N K D L V F M D M K K L A Q Majority	
445	F S Q L R T I S K A D A A S E E L G F K	505	P Y S Q L G N K D L A F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
D A A D H P - D D A T Q C L F G E E L S Majority		F L A G K P E H P M T R E T L N A E N I Majority	
465	D A A D H P - D D A T Q C L F G E E L S	525	F L A G K P E H P M T R E T L N A E N I
492	D A A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
492	D A A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
492	D A A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
L T S S V Q Q V I G L A G K A T D M S E Majority		A K Y A F R I V P - Majority	
485	L S N P D Q Q V I G L A G N P T D T S Q	545	A K Y A F R I V P .
511	L T S S D Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .
511	L T S S V Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .
511	L T S S V Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .

FIG. 7E

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**FIG. 8**



**FIG. 9A**

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Putative Hrp-box

```

1  ACAGTTCCCCAGGGTGAATAGGGAAAGGTGTGATGgaagccttttcgtgctcttttgcgcag
61  ACAGCGCTGATCTTGCGGGTGATTCCGGTCCGCAGGCAGAAGATCGGAGAGGATCAGCAT
121  ATGGCGGGTATCAATAGAGCGGGACCATCGGGCGCTTATTTTGTGTCACACAGACCCC
1  M A G I N R A G P S G A Y F V G H T D P
181  GAGCCAGTATCGGGGCAAGCACACGGATCCGGCAGCGGCCAGCTCCTCGAACAGTCCG
21  E P V S G Q A H G S G S G A S S S N S P
241  CAGGTTACGCCGACCCCTCGAATACTCCCCCGTCGAACGCGCCCCACCGCGCCCAACC
41  Q V Q P R P S N T P P S N A P A P P P T
301  GGACGTGAGAGGCTTTCACGATCCACGGCGCTGTCGCGCCAAACCAGGGAGTGGCTGGAG
61  G R E R L S R S T A L S R Q T R E W L E
361  CAGGGTATGCCTACAGCGGAGGATGCCAGCGTCGTCGTAGGCCACAGGTGACTGCCGAT
81  Q G M P T A E D A S V R R R P Q V T A D
421  GCCGCAACGCCGCGTGCAGAGGCAAGACGCACGCCGGAGGCAACTGCCGATGCCAGCGCA
101  A A T P R A E A R R T P E A T A D A S A
481  CCGCGTAGAGGGGCGGTTGCACACGCCAAGATCGTTTCAGCAATGTCAGTGAAGGGC
121  P R R G A V A H A N S I V Q Q L V S E G
541  GCTGATATTTGCGATACTCGTAACATGCTCCGCAATGCAATGAATGCGCAGCGAGTCCGT
141  A D I S H T R N M L R N A M H G D A V A
601  TTTTCTCGAGTAGAACAGAACATATTTTCGCCAGCATTTCCCGAACATGCCCATGCATGGA
161  F S R V E Q N I F R Q H F P N M P M H G
661  ATCAGCCGAGATTCCGAACCTCGATATCGAGCTCCGTGGGGCGCTTCGTCGAGCGGTTAC
181  I S R D S E L A I E L R G A L R A V H
721  CAACAGGCGGGCGTCAGCGCCAGTGAGGTGCCCCACGCCAACACCGGCCAGCCCTGCGGCA
201  Q Q A A S A P V R S P T P T P A S P A A
781  TCATCATCGGGCAGTCAGCGCTTATTGACGGTTTGGCCGTTTGCCTTGTATGGCGCCA
221  S S S G S S Q R S L F G R F A R L M A P
841  AACCAGGACGGTCTGCAACACTGCCGCCTCTCAGACGCCGGTGCAGAGGAGCCCGCCA
241  N O G R S S N T A A S Q T P V D R S P P
901  CGCGTCAACCAAAGACCCATACGCTCGACAGGGCTGCGATGCGTAATCGTGGCAATGAC
261  R V N O R P I R V D R A A M R N R G N D
961  GAGGCGGACGCCGCGGCTGCGGGGTTAGTACAACAGGGGGTCAATTTAGAGCCCTGCGC
281  E A D A A L R G L V Q Q G V N L E H L R
1021  ACGGCCCTTGAAAGACATGTAATGCAGCGCCTCCCTATCCCCCTCGATATAGGCAGCGG
301  T A L E R H V M Q R L P I P L D I G S A
1081  TTGAGAATGTGGGAATTAACCAAGTATCGACTTGGGGGAAAGCCTTGTGCAACATCCC
321  L O N V G I N P S I D L G E S L V Q H P
1141  CTGCTGAATTTGAATGTAGCGTTGAATCGCATGCTGGGGCTGCGTCCCAGCGCTGAAAGA
341  L L N V A L N R M L G L R P S A E R
1201  GCGCCTCGTCCAGCGCTCCCGTCCCGGACCGCCTCCAGGCGACCGGATGGTACG
361  A P R P A V P V A P A T A S R R P D G T
1261  CGTGCAACACGATTGCGGGTGATGCCGGAGCGGGAGGATTACGAAAATAATGTGGCTTAT
381  R A T R L R V M P E R E D Y E N N V A Y
1321  GGAGTGGCTTGCTTAACCTGAACCCGGGGTGGGGGTAAGGCAGGCTGTTGCGGCCTTT
401  G V R L L N L N P G V G V R Q A V A A F
1381  GTAACCGACCGGGCTGAGCGGCCAGCTGGTGGCTAATATCCGGGCAGCCCTGGACCCCT
421  V T D R A E R P A V V A N I R A A L D P
1441  ATCGCGTCACAATTCAGTCAGCTGCCACAATTTCAAGGCCGATGCTGAATCTGAAGAG
441  I A S Q F S Q L R T I S K A D A E S E E
1501  CTGGGTTTAAAGGATGCGGCAGATCATCACCGATGACGTGACGCACTGCTCTTTTGGC
461  L G F K D A A D H H T D D V T H C L F G
1561  GGAGAATTGTCGCTGAGTAATCCGGATCAGCAGGTGATCGGTTTGGCGGGTAATCCGACG
481  G E L S L S N P D Q Q V I G L A G N P T
1621  GACACGTCGCAGCCTTACAGCCAAGAGGGAATAAGGACCTGGCGTTTCATGGATATGAAA
501  D T S Q P Y S Q E G N K D L A F M D M K
1681  AAAGTTGCCCAATTCCTCGCAGGCAAGCTGAGCATCCGATGACCAGAGAAACGCTTAAC
521  K L A Q F L A G K P E H P M T R E T L N
1741  GCCGAAAATATCGCCAAGTATGCTTTTAGAATAGTCCCCTgaCCGCGCTGACAGCTAAAA
541  A E N I A K Y A F R I V P
1801  GCGCATCAAGCTAGCGCCGACAGCGCTCACTGCCACTTCGAAGGTGCGCGTGGAAGCTC
1861  CCGAGTCACGGAATTCGCACCTGCGTCAGGGCTCAGTCCATGCGCTCGGGGTAGGTCATC

```

FIG. 9B

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- 52% identity of amino acid between AvrPtoB and VirPphA
- Black boxed letters: Putative hrp-box

- Red boxed letters: Computer suggested N-myristoylation site

1.	3- 8	GINRAG
2.	25- 30	GQAHGS
3.	29- 34	GSGSGA
4.	31- 36	GSGASS
5.	33- 38	GASSSN
6.	82- 87	GMPTAE
7.	140-145	GADISH
8.	278-283	GNDEAD
9.	288-293	GVSTTG
10.	294-299	GQFRAL
11.	325-330	GINPSI
12.	353-358	GLRPSA
13.	379-384	GTRATR
14.	412-417	GVRQAV
15.	480-485	GGELSL

- Black bold letters: Amino acid identical with amino acid of VirPphA

- Blue arrow: Fusion point of truncated AvrPtoB with LexA of prey vector

1.	70 AA; <i>HinP1I</i>
2.	112 AA; <i>MspI</i>
3.	121 AA; <i>AclI</i>

**FIG. 9B (CONT.)**

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## ALIGNMENT OF THE AMINO ACID SEQUENCES OF AvrPtoB AND VirPpha

## BlastX results

Sequences producing significant alignments:					Score	E
					(bits)	Value
gi	5702216	gb	AAD47203.1	AF141883_1 (AF141883) VirPpha [Pse...	500	e-140
gi	5702219	gb	AAD47206.1	AF141883_4 (AF141883) unknown [Pse...	70	6e-11
gi	7512219	pir	T18535	high molecular mass nuclear antigen ...	50	6e-05
gi	15236788	ref	NP_194968.1	(NC_003075) putative protein [...	45	0.002
gi	5420387	emb	CAB46679.1	(AJ243459) proteophosphoglycan [...	45	0.003
gi	6322209	ref	NP_012284.1	(NC_001141) Required for invasi...	44	0.005
gi	14251109	ref	NP_116471.1	(NC_002794) t120 [Tupaia herpe...	43	0.008
gi	4507349	ref	NP_003176.1	(NM_003185) TATA box binding pr...	42	0.013
gi	17546705	ref	NP_520107.1	(NC_003295) PROBABLE TRANSMENB...	42	0.013
gi	15805485	ref	NP_294181.1	(NC_001263) hypothetical prote...	42	0.013
gi	17487943	ref	XP_036528.2	(XM_036528) serine/arginine re...	42	0.018

>gi|5702216|gb|AAD47203.1|AF141883\_1 (AF141883) VirPpha [Pseudomonas syringae pv. phaseolicola] Length = 539

Score = 500 bits (1287), Expect = e-140  
 Identities = 303/581 (52%), Positives = 368/581 (63%), Gaps = 28/581 (4%)  
 Frame = +1

Query: 1 MAGINRAGPSGAYFVGHTDPEFVSGQAHSGSGGASSNSPQVQPRPSNTPPSNAPAPPT 180  
 MGIN AGPS ++ TD EPV+ + H S ASS+NSP++ P S P +  
 Sbjct: 1 MPGINGAGPSNFFWQWRTDGEFVTEREHDSSRSASSANSPELPPAS-----PAES 51

Query: 183 GRERLSRSTALSRQTREMLEQGMPTAEDASVRRRPQVTADAATPRAEARRTPEATADASA 360  
 GR+RL RS+ALSRQTREMLE A A V+ ATP AEAR++PEA  
 Sbjct: 52 GRQRLLRSEALSRQTREMLE-----ATPARVQ-----GATPPAEARQSPEAQ----- 93

Query: 361 PRGAVAHANSIVQQLVSEGADISHTRMLRNAMNGDAVAFSRVEQNIHQHFFPMQPMHG 540  
 A IVQ+LV GAD+++ R MLRN M+ +AVAFSRVE++I QHFFPMQPM G  
 Sbjct: 94 -----QAERIVQELVRGGADLNNVRLMLRNVMIDNDAVAFSRVERDILLQHFFPMQPMTG 146

Query: 541 ISRDSELAIELRGALRRRAVHQQAASAPVRSPTTTPASPAASSSGSSQSLFGRFARLMAP 720  
 IS DS LA ELR LR+ V QQ R+ TPA A SSSGSSQSL GR LM P  
 Sbjct: 147 ISSDSVLANELRQRLRQTVRQQ-----RIQSSTPARLADSSSGSSQSLIGRSTMLMTP 200

Query: 721 NQGRSSNTAASQTPVDRSPFRVNQRPIRVDRAMRNNGNDEADAALRGLVQQGVNLEHLR 900  
 + SS+ AAS+T VDR P ++ R+ AA N ++ + ALR L Q+GV++E LR  
 Sbjct: 201 GRSSSSSAAASRTSVDHRHPQGLDLESARLASAARHNSANQTNEALRRLTQEGVIMERLR 260

Query: 901 TALERHVMQRLPIPLDIGSALQNVGINPSIDLGESLVQHPLLNINLVALNRMGLRPSAER 1080  
 T+L R++M P+P D+ AL++VGINP I SLV HP+LN + ALNRML R +  
 Sbjct: 261 TELGRYIMSLEPLPPDLRRALRESVGINPFIPEELSLVDHPVLNFSALNRMGLASRQTTN 320

Query: 1081 APRPAVPVAPATASRR-----PDGT---RATRLRVMPERE 1176  
 +P + A + RR P + RA RL VMP +  
 Sbjct: 321 SPELPPLASSAESGRRRLRLSPPLLSGQREWIEQSMRQAEFQSSRLNRAVRLAVMPQN 380

Query: 1177 DYENNVAYGVRLNLNPGVGVRQAVAFVTDRAERPAVVANIRAALDPIASQFSQSLRTIS 1356  
 + E+NVAY +RL LNPG V + VA+P+TD A R VV +IRAALD IA QFSQSLRTIS  
 Sbjct: 381 ENEDNVAYAIRLRLNPGADVSRVVASFITDPAARQVVDIRAALD-IAPQFSQSLRTIS 439



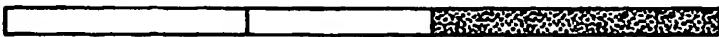




Query: 1357 KADAESEELGPKDAADHHTDDVTHCLFGGELSLSNPDQVIGLAGNPTDTSQPYSEQBNK 1536  
 KADAESEELGP+DAAD H D+ T CLFG ELSLSNPDQVIGLA NPTD QPYSEQ NK  
 Sbjct: 440 KADAESEELGPRDAAD-HPDNATSCFLGGEELSLSNPDQVIGLAVNPTDKPQPYSEQEVNK 498

Query: 1537 DLAFMDNKKLAQFLAGKPEHPMTRETNAENIAYAFRIVP 1659  
 L FMDNKKLAQ+LA KPEHP+ R+ L+A+NIAYAP+IVP  
 Sbjct: 499 ALTFMDNKKLAQVLADKPEHPMLNRQRLDAKNIAKYAFKIVP 539


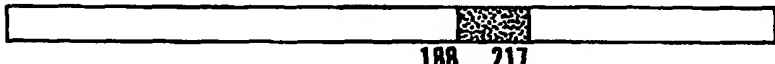
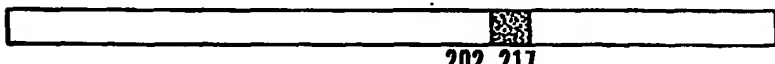
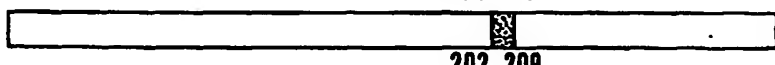
FIG. 9C
















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	CHIMERIC	INTERACTION WITH:	
		AvrPto	AvrPtoB
A		YES	YES
B		NO	NO
D		NO	NO
E		NO	NO
F		NO	NO
G		YES	YES
H		NO	NO

**FIG. 10A**

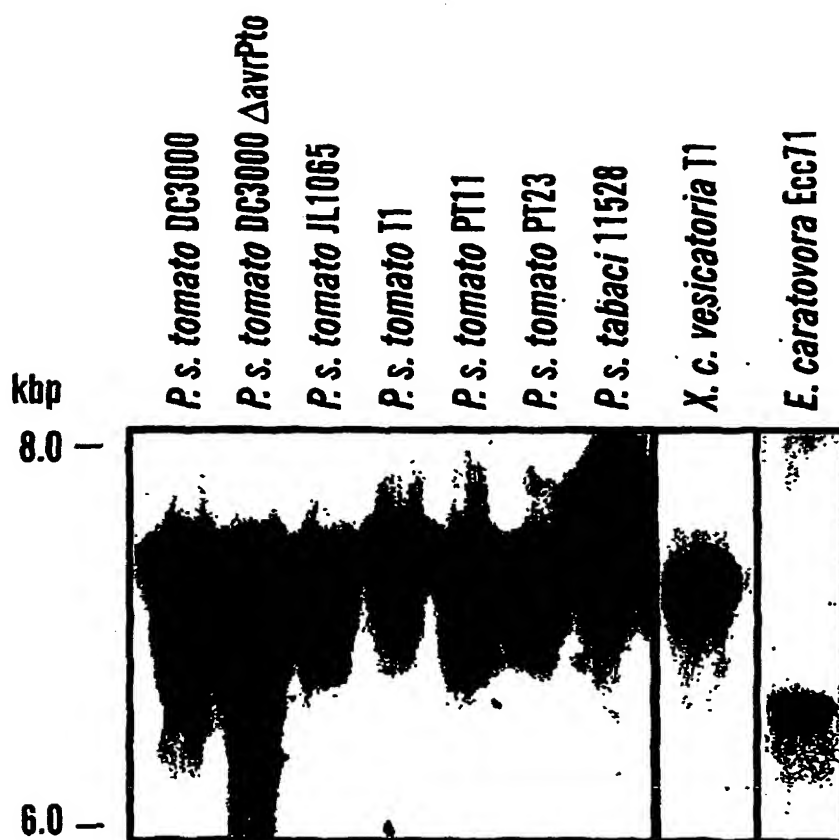
		INTERACTION WITH:	
		AvrPto	AvrPtoB
FPB		YES	YES
FPB2		YES	YES
FPB3		YES	YES
FPB4		YES	YES

**FIG. 10B**

		INTERACTION WITH:	
		AvrPto	AvrPtoB
Pto		YES	YES
Fen		NO	NO
FPB3		YES	YES
FPB4		YES	YES
FPB3(K202R)		YES	YES
FPB3(T204N)		NO	NO
FPB3(L205I)		YES	YES
FPB3(D209A)		YES	YES
P(T204N)		NO	NO
P(L205I)		YES	YES
F(N204T,1205L)		YES	YES
F(N204T)		YES	YES
F(1205L)		NO	NO

**FIG. 10C**

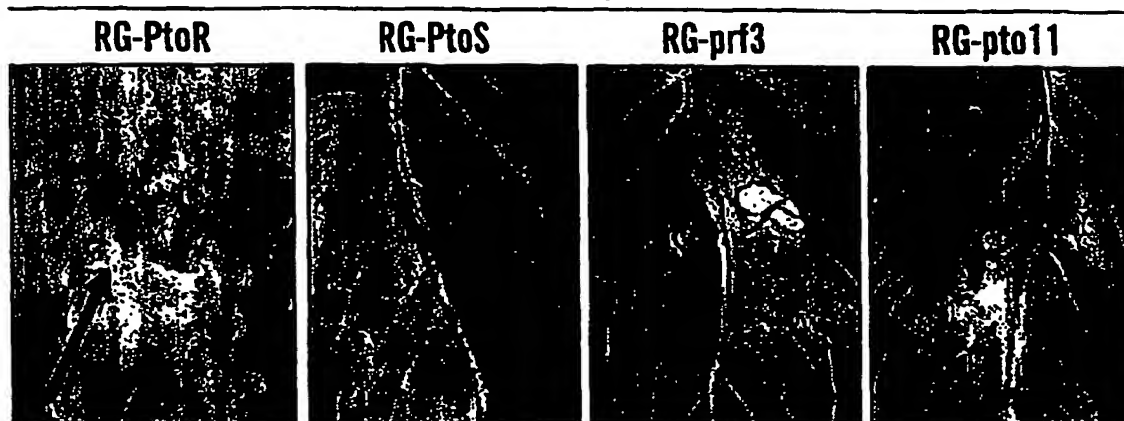
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**FIG. 11**

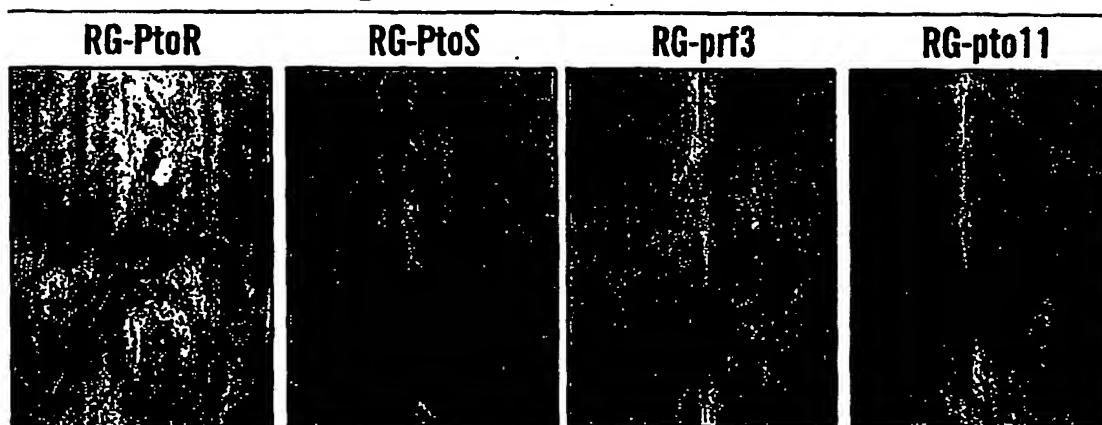
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*P. fluorescens* (Hrp+, avrPtoB)

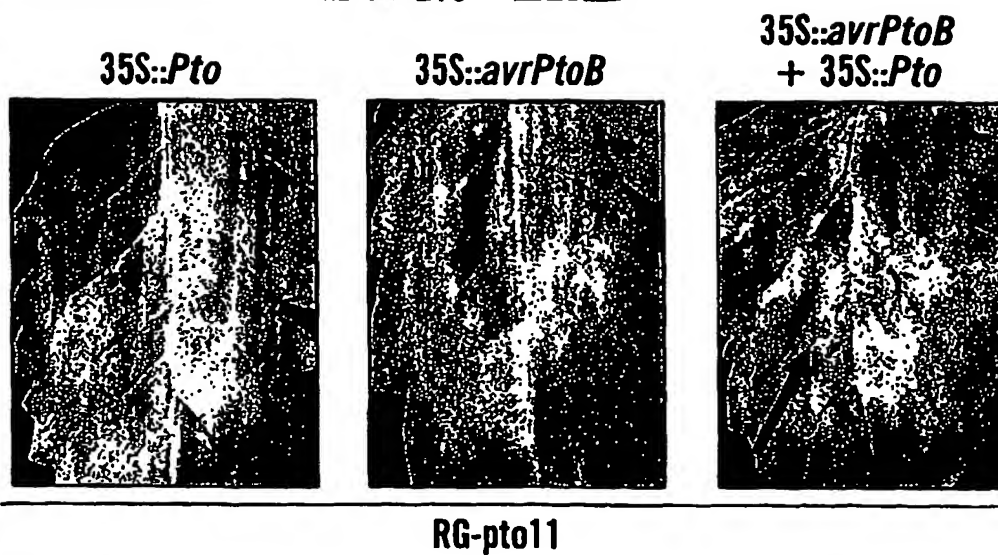


**FIG. 12A**

*Agrobacterium* (35S::avrPtoB)



**FIG. 12B**



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Subregion

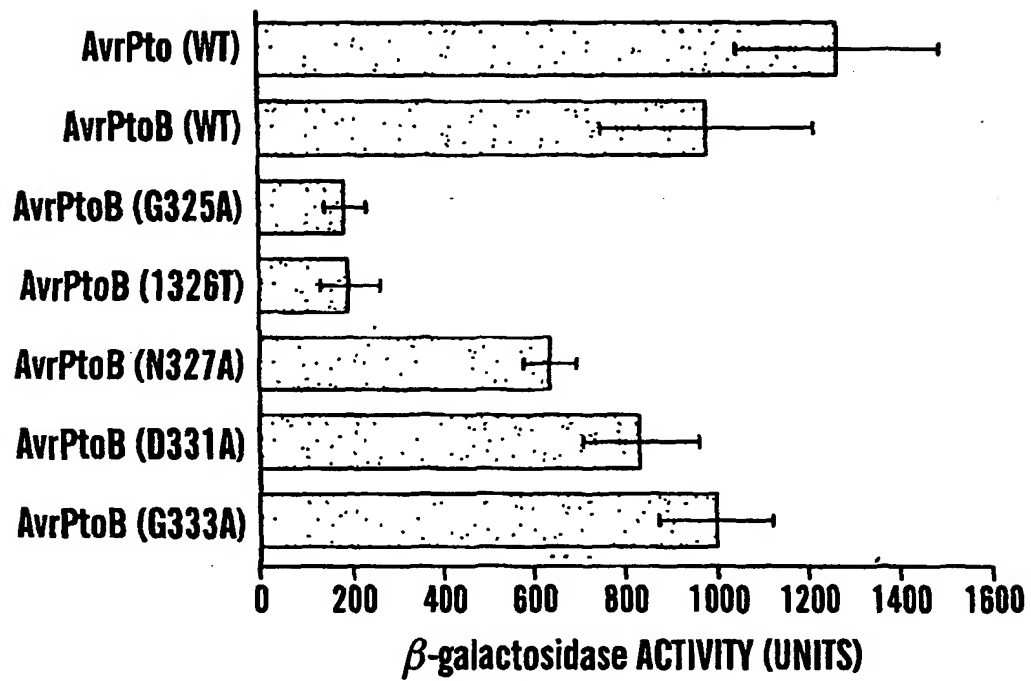
MAGINRAGPSGAYFVGHTDPEFVSGQAHGSGSGASSNSPQVQPRPSNTP MGNICVGG-----SRMAHQVNSPDRVSNNSGDE	I, II
PSNAPAPPPTGRERLSRSTALSRQTREWLEQGMPAEDASVRRRPQVTAD DNVTSSQLLSVRHQLAESAGLPRDQHEFVSSQAP----QSLRNR----- NA121↓ AATPRAEARRTPEATADASAPRRGAVAHANSIVQQLVSEGADISHTRNML -----YNNL-----	III
RNAMNGDAVAFSRVEQNIIFRQHFPNMFHGISRDSELAIELRGALRRVH -----YSHQTORTLDMADMQHRYMTGAS----- ●	IV
QQAASAFVRSPTPTPASPAASSSGSSQRSIFGRFARLMAPNQGRSSNTAA -----	
SQTPVDRSPFRVNQRPIRVDRAMRNRGNDADAALRGLVQQGVNLEHLR -----	
TALERHVMQRLPIPLDIGSALQNVGINPSIDLGESLVQHPLLNLNVALNR -----GINP-----GMLPHENV----- ● ●	V
MLGLRPSAERAPRPAVFPVAPATASRRPDGTRATRLRVMPEREDYENNVAY --DMR-SAITDW-----	VI
GVRLNLNPGVGVRQAVAAVFTDRAERPAAVANIRAALDPIASQFSQLRT -----SDMREAL-----	VII
ISKADAESEELGFKDAADHHTDDVTHCLFGGELSLSNPDQQVIGLAGNPT -----QHANGIHADIP----- ↑ CA40	VIII
DTSQPYSEQGNKDLAFMDMKKLAQFLAGKPEHPMTRETNAE . . . PSPERFVATMN-----PSGSIRMSTLSPS . . .	IX

**FIG. 13A**

Consensus:	SxRxxLxxSxxLxRxxE
AvrPto 38	SVRHQLAESAGLPRDQHE 55
AvrPtoB 60	TGRERLSRSTALSRQTRE 77
VirPphA 51	SGRQRLLRSSALSRQTRE 68
AvrRpt2 49	ETRALLATKTVLGRHKIE 66
AvrRps4 38	TTTSIAQASEGLQRPAT 55
AvrKa10 61	SPAFSAGSFGDLLRQFDP 78
AvrPpiB 41	IEEHVADRLSDLGRPDGG 58
AvrPphF 33	VGQYTLTSIHQLSSEERE 50
AvrBs1 49	RKRVIKENIAALHTSSLE 69
AvrB 33	SQRQLEVYDQCLIGAARW 50
AvrBsT 42	SPSQTSSAFSGLPERPRK 59

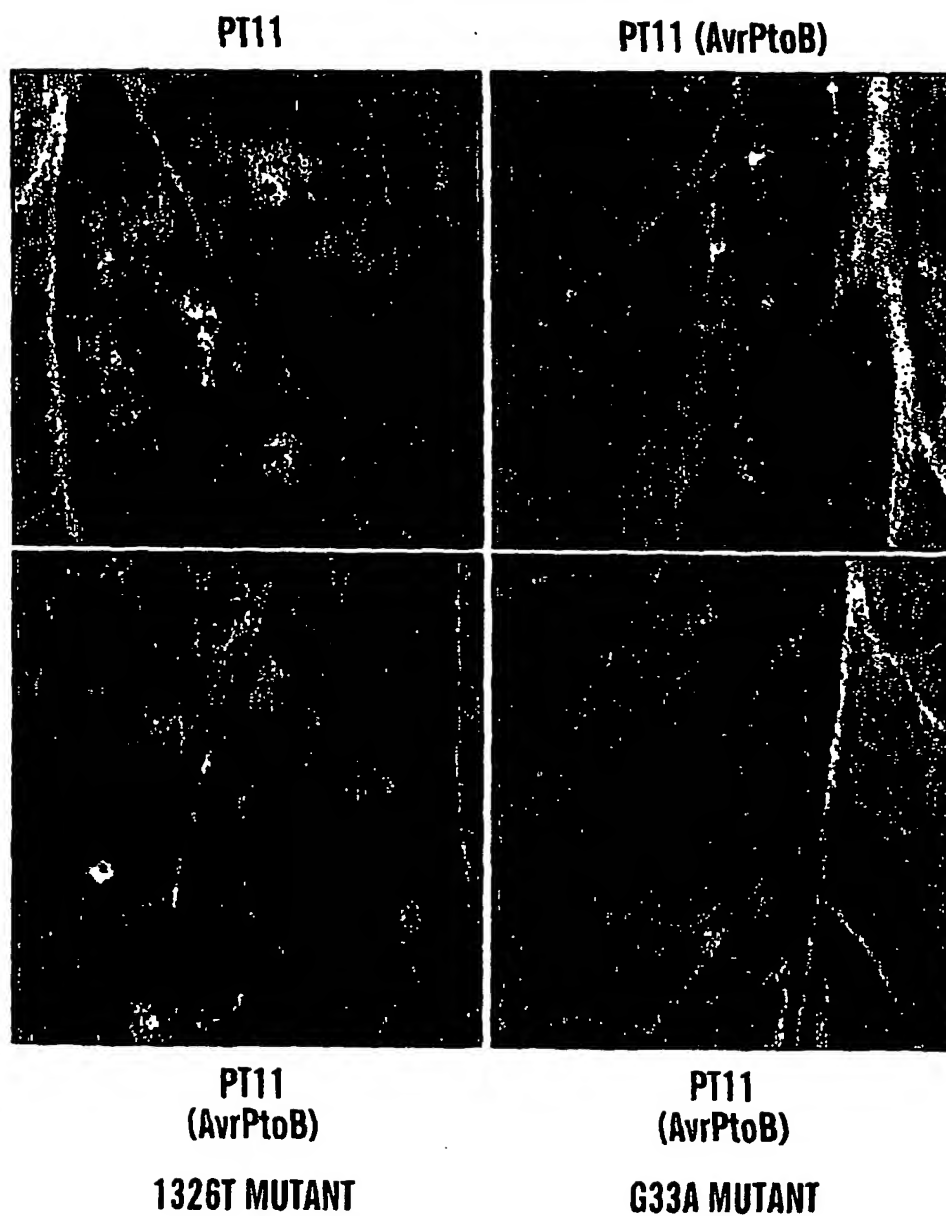
**FIG. 13B**

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**FIG. 14**

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ALL LEAVES ARE Rio-Grande PtoR(*Pto*/*Pto*)

**FIG. 15**

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